

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=1; day=6; hr=15; min=23; sec=26; ms=293;]

=====

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=1; day=6; hr=15; min=19; sec=30; ms=812;]

=====

Application No: 10540394 Version No: 3.0

Input Set:**Output Set:**

Started: 2009-12-17 16:24:08.581
Finished: 2009-12-17 16:24:11.528
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 947 ms
Total Warnings: 25
Total Errors: 0
No. of SeqIDs Defined: 25
Actual SeqID Count: 25

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2009-12-17 16:24:08.581
Finished: 2009-12-17 16:24:11.528
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 947 ms
Total Warnings: 25
Total Errors: 0
No. of SeqIDs Defined: 25
Actual SeqID Count: 25

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 402	Undefined organism found in <213> in SEQ ID (22)
W 402	Undefined organism found in <213> in SEQ ID (23)
W 402	Undefined organism found in <213> in SEQ ID (24)
W 402	Undefined organism found in <213> in SEQ ID (25)

SUBSTITUTE SEQUENCE LISTING

<110> Takeda Pharmaceutical Company Limited

<120> Novel protein and its use

<130> 3132WOOP

<140> 10540394

<141> 2005-09-01

<150> JP2002-378052

<151> 2002-12-26

<150> JP2003-65497

<151> 2003-03-11

<160> 25

<210> 1

<211> 837

<212> PRT

<213> Human

<400> 1

Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro Trp
5 10 15
Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu Leu Leu Leu
20 25 30
Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser Pro Arg Ile
35 40 45
Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu Arg Phe Glu Ala
50 55 60
Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu Ser Arg Asp Gly Arg
65 70 75 80
Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Leu Ser Ser Asn
85 90 95
Leu Ser Phe Leu Pro Gly Gly Glu Tyr Gln Glu Leu Leu Trp Gly Ala
100 105 110
Asp Ala Glu Lys Lys Gln Gln Cys Ser Phe Lys Gly Lys Asp Pro Gln
115 120 125
Arg Asp Cys Gln Asn Tyr Ile Lys Ile Leu Leu Pro Leu Ser Gly Ser
130 135 140
His Leu Phe Thr Cys Gly Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr
145 150 155 160
Ile Asn Met Glu Asn Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val
165 170 175
Leu Leu Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys
180 185 190
Ser Thr Ala Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser
195 200 205
Ser Phe Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg
210 215 220
Pro Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe
225 230 235 240
Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly Asp
245 250 255

Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu	Phe	Glu	260	265	270
Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile	Cys	Lys	Gly	275	280	285
Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp	Thr	Ser	Phe	Leu	290	295	300
Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp	Gly	Phe	Pro	Phe	Asn	305	310	315
Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro	Ser	Pro	Gln	Asp	Trp	Arg	325	330	335
Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr	Ser	Gln	Trp	His	Arg	Gly	Thr	340	345	350
Thr	Glu	Gly	Ser	Ala	Val	Cys	Val	Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	355	360	365
Val	Phe	Ser	Gly	Leu	Tyr	Lys	Glu	Val	Asn	Arg	Glu	Thr	Gln	Gln	Met	370	375	380
Val	His	Arg	Asp	Pro	Pro	Val	Pro	Thr	Pro	Arg	Pro	Gly	Ala	Cys	Ile	385	390	395
Thr	Asn	Ser	Ala	Arg	Glu	Arg	Lys	Ile	Asn	Ser	Ser	Leu	Gln	Leu	Pro	405	410	415
Asp	Arg	Val	Leu	Asn	Phe	Leu	Lys	Asp	His	Phe	Leu	Met	Asp	Gly	Gln	420	425	430
Val	Arg	Ser	Arg	Met	Leu	Leu	Leu	Gln	Pro	Gln	Ala	Arg	Tyr	Gln	Arg	435	440	445
Val	Ala	Val	His	Arg	Val	Pro	Gly	Leu	His	His	Thr	Tyr	Asp	Val	Leu	450	455	460
Phe	Leu	Gly	Thr	Gly	Asp	Gly	Arg	Leu	His	Lys	Ala	Val	Ser	Val	Gly	465	470	475
Pro	Arg	Val	His	Ile	Ile	Glu	Glu	Leu	Gln	Ile	Phe	Ser	Ser	Gly	Gln	485	490	495
Pro	Val	Gln	Asn	Leu	Leu	Leu	Asp	Thr	His	Arg	Gly	Leu	Leu	Tyr	Ala	500	505	510
Ala	Ser	His	Ser	Gly	Val	Val	Gln	Val	Pro	Met	Ala	Asn	Cys	Ser	Leu	515	520	525
Tyr	Arg	Ser	Cys	Gly	Asp	Cys	Leu	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala	530	535	540
Trp	Ser	Gly	Ser	Ser	Cys	Lys	His	Val	Ser	Leu	Tyr	Gln	Pro	Gln	Leu	545	550	555
Ala	Thr	Arg	Pro	Trp	Ile	Gln	Asp	Ile	Glu	Gly	Ala	Ser	Ala	Lys	Asp	565	570	575
Leu	Cys	Ser	Ala	Ser	Ser	Val	Val	Ser	Pro	Ser	Phe	Val	Pro	Thr	Gly	580	585	590
Glu	Lys	Pro	Cys	Glu	Gln	Val	Gln	Phe	Gln	Pro	Asn	Thr	Val	Asn	Thr	595	600	605
Leu	Ala	Cys	Pro	Leu	Leu	Ser	Asn	Leu	Ala	Thr	Arg	Leu	Trp	Leu	Arg	610	615	620
Asn	Gly	Ala	Pro	Val	Asn	Ala	Ser	Ala	Ser	Cys	His	Val	Leu	Pro	Thr	625	630	635
Gly	Asp	Leu	Leu	Leu	Val	Gly	Thr	Gln	Gln	Leu	Gly	Glu	Phe	Gln	Cys	645	650	655
Trp	Ser	Leu	Glu	Glu	Gly	Phe	Gln	Gln	Leu	Val	Ala	Ser	Tyr	Cys	Pro	660	665	670
Glu	Val	Val	Glu	Asp	Gly	Val	Ala	Asp	Gln	Thr	Asp	Glu	Gly	Gly	Ser	675	680	685
Val	Pro	Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly	690	695	700
Lys	Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val			

705					710				715				720			
Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe	Leu	
				725				730				735				
Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln	Gly	Glu	
				740				745				750				
Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu	Pro	Pro	Glu	
				755				760				765				
Thr	Arg	Pro	Leu	Asn	Gly	Leu	Gly	Pro	Pro	Ser	Thr	Pro	Leu	Asp	His	
				770				775				780				
Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro	Gly	Ser	Arg	Val	Phe	
785				790				795				800				
Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	Ile	Gln	Asp	Ser	Phe	Val	Glu	
				805				810				815				
Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg	Val	Arg	Leu	Gly	Ser	Glu	Ile	
				820				825				830				
Arg	Asp	Ser	Val	Val												
				835												

atgtctgcgca	ccgcgatggg	cctgaggagc	tggctcgcgc	ccccatgggg	cgcgctgccg	60
cctcgggcac	cgctgctgct	gctcctgctg	ctgctgctcc	tgctgcagcc	gccgcctccg	120
acctggggcg	tcagcccccg	gatcagcctg	cctctgggct	ctgaagagcg	gccattcctc	180
agattcgaag	ctgaacacat	ctccaactac	acagcccttc	tgctgagcag	ggatggcagg	240
accctgtacg	tgggtgctcg	agaggccctc	tttgactctc	gtagcaacct	cagcttcctg	300
ccaggcgggg	agtaccagga	gctgctttgg	ggtgcagacg	cagagaagaa	acagcagtgc	360
agcttcaagg	gcaaggaccc	acagcgcgac	tgtcaaaact	acatcaagat	cctcctgccg	420
ctcagcggca	gtcacctgtt	cacctgtggc	acagcagcct	tcagccccaat	gtgtacctac	480
atcaacatgg	agaacttcac	cctggcaagg	gacgagaagg	ggaatgtcct	cctggaagat	540
ggcaaggggc	gttgtccctt	cgaccgcaat	ttcaagtcca	ctgccctggt	ggttgatggc	600
gagctctaca	ctggaacagt	cagcagcttc	caagggaatg	acccggccaat	ctcgcggagc	660
caaagccttc	gccccacca	gaccgagagc	tcctcaact	ggctgcaaga	cccagctttt	720
gtggcctcag	cctacatttc	tgagagcctg	ggcagcttgc	aaggcgatga	tgacaagatc	780
tactttttct	tcagcgagac	tggccaggaa	tttgagttct	ttgagaacac	catttgtgtcc	840
cgcattgccc	gcatctgcaa	ggcgatgag	ggtggagagc	gggtgctaca	gcagcgctgg	900
acctccttcc	tcaaggccca	gctgctgtgc	tcacggcccg	acgatggctt	ccccttcaac	960
gtgctgcagg	atgtcttcac	gctgagcccc	agccccagg	actggcgtga	caccttttcc	1020
tatggggtct	tactttccca	gtggcacagg	ggaactacag	aaggctctgc	cgtctgtgtc	1080
ttcacaatga	aggatgtgca	gagagtcttc	agcggcctct	acaaggaggt	gaaccgtgag	1140
acacagcaga	tggtacaccg	tgaccacccc	gtgcccacac	cccggcctgg	agcgtgcatc	1200
accaacagtg	cccgggaaag	gaagatcaac	tcatccctgc	agctcccaga	ccgcgtgctg	1260
aactttctca	aggaccactt	cctgatggac	gggcaggtcc	gaagccgcat	gctgctgctg	1320
cagccccagg	ctcgctacca	gcgcgtggct	gtacaccgcg	tccttgccct	gcaccacacc	1380
tacgatgtcc	tcttcttggg	cactggtgac	ggccggtccc	acaaggcagt	gagcgtgggc	1440
ccccgggtgc	acatcattga	ggagctgcag	atcttctcat	cgggacagcc	cgtgcagaat	1500
ctgctcctgg	acacccacag	ggggctgctg	tatgcggcct	cacactcggg	cgtagtccag	1560
gtgcccatgg	ccaactgcag	cctgtaccgg	agctgtgggg	actgcctcct	cgccccggac	1620
ccctactgtg	cttggaaggc	ctccagctgc	aagcacgtca	gcctctacca	gcctcagctg	1680
gccaccaggc	cgtggatcca	ggacatcgag	ggagccagcg	ccaaggacct	ttgcagcgcg	1740
tcttcggttg	tgtccccgtc	ttttgtacca	acaggggaga	agccatgtga	gcaagtccag	1800
ttccagccca	acacagtga	cactttggcc	tgcccgtccc	tctccaacct	ggcgaccgga	1860
ctctggctac	gcaacggggc	ccccgtcaat	gcctcggcct	cctgccacgt	gctacccaact	1920

ggggacctgc	tgctggtggg	cacccaacag	ctgggggagt	tccagtgtctg	gtcactagag	1980
gagggcttcc	agcagctggt	agccagctac	tgcccagagg	tggtggagga	cggggtggca	2040
gaccaaacag	atgaggggtg	cagtgtaccc	gtcattatca	gcacatcgcg	tgtgagtgca	2100
ccagctggtg	gcaaggccag	ctgggggtgca	gacaggtcct	actggaagga	gttcctggtg	2160
atgtgcacgc	tctttgtgct	ggcgtgtctg	ctcccagttt	tattcttgc	ctaccggcac	2220
cggaacagca	tgaagtctt	cctgaagcag	ggggaatgtg	ccagcgtgca	ccccaagacc	2280
tgcctgtgg	tgtgcccc	tgagaccgc	ccactcaacg	gcctagggcc	ccctagcacc	2340
ccactcgatc	accgagggtg	ccagtccctg	tcagacagcc	ccccggggc	ccgagtcttc	2400
actgagtcag	agaagaggcc	actcagcatc	caagacagct	tcgtggaggt	atccccagtg	2460
tgcccccggc	cccggtccg	ccttggtctg	gagatccgtg	actctgtggt	g	2511

<210> 3

<211> 3766

<212> DNA

<213> Human

<400> 3

gctctgccca	agccgaggct	gcggggcgcg	cgccggcggg	aggactgcgg	tgcccccgcg	60
aggggctgag	tttgccagg	cccacttgac	cctgtttccc	acctcccgc	ccccaggtcc	120
ggaggcggg	gccccgggg	cgactcggg	gcggaccgcg	gggcggagct	gccgcccgtg	180
agtccggccg	agccacctga	gcccagaccg	cgggacaccg	tcgtcctgc	tctccgaatg	240
ctgcgccaccg	cgatgggct	gaggagctgg	ctgcgccccc	catggggcgc	gctgccgcct	300
cggccaccgc	tgtgtgtgt	cctgtgtgtg	ctgtcctgc	tgacgccgc	gcctccgacc	360
tgggcgctca	gccccggat	cagcctgcct	ctgggctctg	aagagcggcc	attcctcaga	420
ttcgaagctg	aacacatctc	caactacaca	gcccttctgc	tgagcaggga	tggcaggacc	480
ctgtacgtgg	gtgtctcgaga	ggccctcttt	gcactcagta	gcaacctcag	cttctctcca	540
ggcggggagt	accaggagct	gctttgggg	gcagacgcag	agaagaaaca	gcagtgcagc	600
ttcaagggca	aggaccacaca	gcgcgactgt	caaaactaca	tcaagatcct	cctgccgctc	660
agcggcagtc	acctgttcac	ctgtggcaca	gcagccttca	gccccatgtg	tacctacatc	720
aacatggaga	acttcaccct	ggcaagggac	gagaagggga	atgtcctcct	ggaagatggc	780
aaggggccgtt	gtcccttcga	cccgaatttc	aagtccactg	ccctggtggt	tgatggcgag	840
ctctacactg	gaacagtcag	cagcttccaa	gggaatgacc	cggccatctc	gcggagccaa	900
agccttcgcc	ccaccaagac	cgagagctcc	ctcaactggc	tgcaagaccc	agcttttgtg	960
gcctcagcct	acattcctga	gagcctgggc	agcttgcaag	gcgatgatga	caagatctac	1020
tttttcttca	gcgagactgg	ccaggaattt	gagttctttg	agaacaccat	tgtgtccgc	1080
attgcccgca	tctgcaagg	cgatgagggt	ggagagcggg	tgctacagca	gcgctggacc	1140
tccttcctca	aggcccagct	gctgtgtctca	cggcccgacg	atggcttccc	cttcaacgtg	1200
ctgcaggatg	tcttcacgct	gagccccagc	cccaggact	ggcgtgacac	ccttttctat	1260
ggggtcttca	cttcccagtg	gcacagggga	actacagaag	gctctgccgt	ctgtgtcttc	1320
acaatgaagg	atgtgcagag	agtcttcagc	ggcctctaca	aggaggtgaa	ccgtgagaca	1380
cagcagatgg	tacaccgtga	cccaccctg	cccacacccc	ggcctggagc	gtgcatcacc	1440
aacagtgcc	gggaaaggaa	gatcaactca	tccttcgagc	tcccagaccg	cgtgctgaac	1500
tttctcaagg	accacttcct	gatggacggg	caggtecgaa	gccgcattgt	gctgctgcag	1560
ccccaggctc	gctaccagcg	cgtggctgta	caccgcgtcc	ctggcctgca	ccacacctac	1620
gatgtcctct	tcctgggcac	tggtgacggc	cggctccaca	aggcagtgag	cgtgggcccc	1680
cgggtgcaca	tcattgagga	gctgcagatc	ttctcatcgg	gacagcccg	gcagaatctg	1740
ctcctggaca	cccacagggg	gctgtgttat	gcggcctcac	actcgggcgt	agtcaggtg	1800
cccatggcca	actgcagcct	gtaccggagc	tgtggggact	gcctcctcgc	ccgggacccc	1860
tactgtgctt	ggagcggctc	cagctgcaag	cacgtcagcc	tctaccagcc	tcagctggcc	1920
accaggccgt	ggatccagga	catcgaggga	gccagcgcca	aggacctttg	cagcgcgtct	1980
tcggttgtgt	ccccgtcttt	tgtaccaaca	ggggagaagc	catgtgagca	agtcagttc	2040
cagcccaaca	cagtgaacac	tttggcctgc	ccgtcctct	ccaacctggc	gacccgactc	2100
tggctacgca	acggggcccc	cgtcaatgcc	tcggcctcct	gccacgtgct	acccactggg	2160
gacctgctgc	tggtgggcac	ccaacagctg	ggggagttcc	agtgtgtgtc	actagaggag	2220
ggcttccagc	agctggtagc	cagctactgc	ccagagggtg	tggaggacgg	ggtggcagac	2280
caaacagatg	aggggtggcag	tgtaccctgc	attatcagca	catcgctgtg	gagtgcacca	2340

```

gctgggtggca aggccagctg ggggtgcagac aggtcctact ggaaggagtt cctgggtgatg 2400
tgcacgctct ttgtgctggc cgtgctgctc ccagttttat tcttgctcta ccggcaccgg 2460
aacagcatga aagtcttcct gaagcagggg gaatgtgcc aagcgtgcaccc caagacctgc 2520
cctgtggtgc tgcacctga gacccgccc ctcaacggcc tagggccccc tagcacccca 2580
ctcgatcacc gagggtagca gtccctgtca gacagccccc cgggggtcccg agtcttcact 2640
gagtcagaga agaggccact cagcatccaa gacagcttcg tggaggtatc cccagtgtgc 2700
ccccggcccc gggtcgcgct tggctcggag atccgtgact ctgtggtgtg agagctgact 2760
tccagaggac gctgccttg cttcaggggc tgtgaatgct cggagagggg caactggacc 2820
tcccctccgc tctgctcttc gtggaacacg accgtggtgc ccggcccttg ggagccttg 2880
ggccagctgg cctgctgctc tccagtcaag tagcgaagct cctaccaccc agacacccaa 2940
acagccgtgg cccagaggt cctggccaaa tatggggggc tgcctagggt ggtggaacag 3000
tgctccttat gtaaactgag ccctttgttt aaaaaacaat tccaaatgtg aaactagaat 3060
gagagggaag agatagcatg gcatgcagca cacacggctg ctccagttca tggcctcca 3120
ggggtgctgg ggatgcatcc aaagtgggtt tctgagacag agttggaac cctcaccaac 3180
tggcctcttc acctccaca ttatcccgct gccaccggct gccctgtctc actgcagatt 3240
caggaccagc ttgggctgcg tgcgttctgc cttgccagtc agccgaggat gtagttgttg 3300
ctgccgtcgt cccaccacct cagggaccag agggctagg tggcactgcg gccctacca 3360
ggctcctggc tcggacccaa ctctggacc tttccagcct gtatcaggct gtggccacac 3420
gagaggacag cgcgagctca ggagagattt cgtgacaatg tacgcctttc cctcagaatt 3480
cagggaagag actgtgcgct gccttcctcc gtgttgctg gagaaccctg gtgcccttc 3540
ccaccatatc caccctcgct ccatctttga actcaaacac gaggaactaa ctgcaccctg 3600
gtcctctccc cagtcaccag ttcacctcc atccctcacc ttcctccact ctaagggata 3660
tcaacactgc ccagcacagg ggccctgaat ttatgtggt tttatacatt ttttaataag 3720
atgcacttta tgtcattttt taataaagtc tgaagaatta ctgttt 3766

```

<210> 4

<211> 837

<212> PRT

<213> Human

<400> 4

```

Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro Trp
      5                      10                      15
Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu Leu Leu
      20                      25                      30
Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser Pro Arg Ile
      35                      40                      45
Ser Leu Pro Leu Gly Ser Glu Arg Pro Phe Leu Arg Phe Glu Ala
      50                      55                      60
Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu Ser Arg Asp Gly Arg
      65                      70                      75                      80
Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Leu Ser Ser Asn
      85                      90                      95
Leu Ser Phe Leu Pro Gly Gly Glu Tyr Gln Glu Leu Leu Trp Gly Ala
      100                     105                     110
Asp Ala Glu Lys Lys Gln Gln Cys Ser Phe Lys Gly Lys Asp Pro Gln
      115                     120                     125
Arg Asp Cys Gln Asn Tyr Ile Lys Ile Leu Leu Pro Leu Ser Gly Ser
      130                     135                     140
His Leu Phe Thr Cys Gly Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr
      145                     150                     155                     160
Ile Asn Met Glu Asn Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val
      165                     170                     175
Leu Leu Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys
      180                     185                     190
Ser Thr Ala Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ile

```

195		200		205	
Ser Phe Gln Gly Asn Asp	Pro Ala Ile Ser Arg	Ser Gln Ser Leu Arg			
210	215	220			
Pro Thr Lys Thr Glu Ser	Ser Leu Asn Trp Leu	Gln Asp Pro Ala Phe			
225	230	235		240	
Val Ala Ser Ala Tyr Ile	Pro Glu Ser Leu Gly	Ser Leu Gln Gly Asp			
245	250	255			
Asp Asp Lys Ile Tyr Phe	Phe Phe Ser Glu Thr	Gly Gln Glu Phe Glu			
260	265	270			
Phe Phe Glu Asn Thr Ile	Val Ser Arg Ile Ala	Arg Ile Cys Lys Gly			
275	280	285			
Asp Glu Gly Gly Glu Arg	Val Leu Gln Gln Arg	Trp Thr Ser Phe Leu			
290	295	300			
Lys Ala Gln Leu Leu Cys	Ser Arg Pro Asp Asp	Gly Phe Pro Phe Asn			
305	310	315		320	
Val Leu Gln Asp Val Phe	Thr Leu Ser Pro Ser	Pro Gln Asp Trp Arg			
325	330				

SUBSTITUTE SEQUENCE LISTING

<110> Takeda Pharmaceutical Company Limited

<120> Novel protein and its use

<130> 3132WOOP

<140> 10540394

<141> 2005-09-01

<150> JP2002-378052

<151> 2002-12-26

<150> JP2003-65497

<151> 2003-03-11

<160> 25

<210> 1

<211> 837

<212> PRT

<213> Human

<400> 1

Met	Leu	Arg	Thr	Ala	Met	Gly	Leu	Arg	Ser	Trp	Leu	Ala	Ala	Pro	Trp	
				5					10					15		
Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu
			20					25					30			
Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser	Pro	Arg	Ile	
		35					40					45				
Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu	Arg	Phe	Glu	Ala	
	50					55					60					
Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu	Ser	Arg	Asp	Gly	Arg	
65				70						75					80	
Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu	Phe	Ala	Leu	Ser	Ser	Asn	
				85					90					95		
Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr	Gln	Glu	Leu	Leu	Trp	Gly	Ala	
			100					105					110			
Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys	Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	
	115					120						125				
Arg	Asp	Cys	Gln	Asn	Tyr	Ile	Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	
	130				135						140					
His	Leu	Phe	Thr	Cys	Gly	Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	
145					150					155					160	
Ile	Asn	Met	Glu	Asn	Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	
			165						170					175		
Leu	Leu	Glu	Asp	Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	
		180						185					190			
Ser	Thr	Ala	Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	
	195					200						205				
Ser	Phe	Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	
	210				215						220					
Pro	Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe	
225				230						235					240	
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly	Asp	
			245						250					255		

Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu	Phe	Glu	260	265	270
Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile	Cys	Lys	Gly	275	280	285
Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp	Thr	Ser	Phe	Leu	290	295	300
Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp	Gly	Phe	Pro	Phe	Asn	305	310	315
Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro	Ser	Pro	Gln	Asp	Trp	Arg	325	330	335
Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr	Ser	Gln	Trp	His	Arg	Gly	Thr	340	345	350
Thr	Glu	Gly	Ser	Ala	Val	Cys	Val	Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	355	360	365
Val	Phe	Ser	Gly	Leu	Tyr	Lys	Glu	Val	Asn	Arg	Glu	Thr	Gln	Gln	Met	370	375	380
Val	His	Arg	Asp	Pro	Pro	Val	Pro	Thr	Pro	Arg	Pro	Gly	Ala	Cys	Ile	385	390	395
Thr	Asn	Ser	Ala	Arg	Glu	Arg	Lys	Ile	Asn	Ser	Ser	Leu	Gln	Leu	Pro	405	410	415
Asp	Arg	Val	Leu	Asn	Phe	Leu	Lys	Asp	His	Phe	Leu	Met	Asp	Gly	Gln	420	425	430
Val	Arg	Ser	Arg	Met	Leu	Leu	Leu	Gln	Pro	Gln	Ala	Arg	Tyr	Gln	Arg	435	440	445
Val	Ala	Val	His	Arg	Val	Pro	Gly	Leu	His	His	Thr	Tyr	Asp	Val	Leu	450	455	460
Phe	Leu	Gly	Thr	Gly	Asp	Gly	Arg	Leu	His	Lys	Ala	Val	Ser	Val	Gly	465	470	475
Pro	Arg	Val	His	Ile	Ile	Glu	Glu	Leu	Gln	Ile	Phe	Ser	Ser	Gly	Gln	485	490	495
Pro	Val	Gln	Asn	Leu	Leu	Leu	Asp	Thr	His	Arg	Gly	Leu	Leu	Tyr	Ala	500	505	510
Ala	Ser	His	Ser	Gly	Val	Val	Gln	Val	Pro	Met	Ala	Asn	Cys	Ser	Leu	515	520	525
Tyr	Arg	Ser	Cys	Gly	Asp	Cys	Leu	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala	530	535	540
Trp	Ser	Gly	Ser	Ser	Cys	Lys	His	Val	Ser	Leu	Tyr	Gln	Pro	Gln	Leu	545	550	555
Ala	Thr	Arg	Pro	Trp	Ile	Gln	Asp	Ile	Glu	Gly	Ala	Ser	Ala	Lys	Asp	565	570	575
Leu	Cys	Ser	Ala	Ser	Ser	Val	Val	Ser	Pro	Ser	Phe	Val	Pro	Thr	Gly	580	585	590
Glu	Lys	Pro	Cys	Glu	Gln	Val	Gln	Phe	Gln	Pro	Asn	Thr	Val	Asn	Thr	595	600	605
Leu	Ala	Cys	Pro	Leu	Leu	Ser	Asn	Leu	Ala	Thr	Arg	Leu	Trp	Leu	Arg	610	615	620
Asn	Gly	Ala	Pro	Val	Asn	Ala	Ser	Ala	Ser	Cys	His	Val	Leu	Pro	Thr	625	630	635
Gly	Asp	Leu	Leu	Leu	Val	Gly	Thr	Gln	Gln	Leu	Gly	Glu	Phe	Gln	Cys	645	650	655
Trp	Ser	Leu	Glu	Glu	Gly	Phe	Gln	Gln	Leu	Val	Ala	Ser	Tyr	Cys	Pro	660	665	670
Glu	Val	Val	Glu	Asp	Gly	Val	Ala	Asp	Gln	Thr	Asp	Glu	Gly	Gly	Ser	675	680	685
Val	Pro	Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly	690	695	700
Lys	Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val			

ggggacctgc	tgctggtggg	cacccaacag	ctgggggagt	tccagtgtctg	gtcactagag	1980
gagggcttcc	agcagctggt	agccagctac	tgcccagagg	tggtggagga	cggggtggca	2040
gaccaaacag	atgaggggtg	cagtgtaccc	gtcattatca	gcacatcgcg	tgtgagtgca	2100
ccagctggtg	gcaaggccag	ctgggggtgca	gacaggtcct	actggaagga	gttcctggtg	2160
atgtgcacgc	tctttgtgct	ggcgtgtctg	ctcccagttt	tattcttgc	ctaccggcac	2220
cggaacagca	tgaagtctt	cctgaagcag	ggggaatgtg	ccagcgtgca	ccccaagacc	2280
tgcctgtgg	tgtgcccc	tgagaccgc	ccactcaacg	gcctagggcc	ccctagcacc	2340
ccactcgatc	accgagggtg	ccagtccctg	tcagacagcc	ccccggggc	ccgagtcttc	2400
actgagtcag	agaagaggcc	actcagcatc	caagacagct	tcgtggaggt	atccccagtg	2460
tgcccccggc	cccggtccg	ccttggtctg	gagatccgtg	actctgtggt	g	2511

<210> 3

<211> 3766

<212> DNA

<213> Human

<400> 3

gctctgccca	agccgaggct	gcggggcgcg	cgccggcggg	aggactgcgg	tgcccccgcg	60
aggggctgag	tttgccagg	cccacttgac	cctgtttccc	acctcccgc	ccccaggtcc	120
ggaggcggg	gccccgggg	cgactcggg	gcggaccgcg	gggcggagct	gccgcccgtg	180
agtccggccg	agccacctga	gcccagaccg	cgggacaccg	tcgtcctgc	tctccgaatg	240
ctgcgccaccg	cgatgggct	gaggagctgg	ctgcgccccc	catggggcgc	gctgccgcct	300
cggccaccgc	tgtgtgtgt	cctgtgtgtg	ctgtcctgc	tgacgccgc	gcctccgacc	360
tgggcgctca	gccccggat	cagcctgcct	ctgggctctg	aagagcggcc	attcctcaga	420
ttcgaagctg	aacacatctc	caactacaca	gcccttctgc	tgagcaggga	tggcaggacc	480
ctgtacgtgg	gtgtctcgaga	ggccctcttt	gcactcagta	gcaacctcag	cttctctcca	540
ggcggggagt	accaggagct	gctttgggg	gcagacgcag	agaagaaaca	gcagtgcagc	600
ttcaagggca	aggaccacaca	gcgcgactgt	caaaactaca	tcaagatcct	cctgccgctc	660
agcggcagtc	acctgttcac	ctgtggcaca	gcagccttca	gccccatgtg	tacctacatc	720
aacatggaga	acttcaccct	ggcaagggac	gagaagggga	atgtcctcct	ggaagatggc	780
aaggggccgtt	gtcccttcga	cccgaatttc	aagtccactg	ccctggtggt	tgatggcgag	840
ctctacactg	gaacagtcag	cagcttccaa	gggaatgacc	cggccatctc	gcggagccaa	900
agccttcgcc	ccaccaagac	cgagagctcc	ctcaactggc	tgcaagaccc	agcttttgtg	960
gcctcagcct	acattcctga	gagcctgggc	agcttgcaag	gcgatgatga	caagatctac	1020
tttttcttca	gcgagactgg	ccaggaattt	gagttctttg	agaacaccat	tgtgtccgc	1080
attgcccgca	tctgcaagg	cgatgagggt	ggagagcggg	tgctacagca	gcgctggacc	1140
tccttcctca	aggcccagct	gctgtgtctca	cggcccgacg	atggcttccc	cttcaacgtg	1200
ctgcaggatg	tcttcacgct	gagccccagc	cccaggact	ggcgtgacac	ccttttctat	1260
ggggtcttca	cttcccagtg	gcacagggga	actacagaag	gctctgccgt	ctgtgtcttc	1320
acaatgaagg	atgtgcagag	agtcttcagc	ggcctctaca	aggaggtgaa	ccgtgagaca	1380
cagcagatgg	tacaccgtga	cccaccctg	cccacacccc	ggcctggagc	gtgcatcacc	1440
aacagtgcc	gggaaaggaa	gatcaactca	tccttcgagc	tcccagaccg	cgtgctgaac	1500
tttctcaagg	accacttcct	gatggacggg	caggtecgaa	gccgcattgt	gctgctgcag	1560
ccccaggctc	gctaccagcg	cgtggctgta	caccgcgtcc	ctggcctgca	ccacacctac	1620
gatgtcctct	tcctgggcac	tggtgacggc	cggctccaca	aggcagtgag	cgtgggcccc	1680
cgggtgcaca	tcattgagga	gctgcagatc	ttctcatcgg	gacagcccg	gcagaatctg	1740
ctcctggaca	cccacagggg	gctgtgttat	gcggcctcac	actcgggcgt	agtcaggtg	1800
cccatggcca	actgcagcct	gtaccggagc	tgtggggact	gcctcctcgc	ccgggacccc	1860
tactgtgctt	ggagcggctc	cagctgcaag	cacgtcagcc	tctaccagcc	tcagctggcc	1920
accaggccgt	ggatccagga	catcgaggga	gccagcgcca	aggacctttg	cagcgcgtct	1980
tcggttgtgt	ccccgtcttt	tgtaccaaca	ggggagaagc	catgtgagca	agtcagttc	2040
cagcccaaca	cagtgaacac	tttggcctgc	ccgtcctct	ccaacctggc	gacccgactc	2100
tggctacgca	acggggcccc	cgtcaatgcc	tcggcctcct	gccacgtgct	acccactggg	2160
gacctgctgc	tggtgggcac	ccaacagctg	ggggagttcc	agtgtgtgtc	actagaggag	2220
ggcttccagc	agctggtagc	cagctactgc	ccagagggtg	tggaggacgg	ggtggcagac	2280
caaacagatg	aggggtggcag	tgtaccctgc	attatcagca	catcgctgtg	gagtgcacca	2340

```

gctgggtggca aggccagctg ggggtgcagac aggtcctact ggaaggagtt cctgggtgatg 2400
tgcacgctct ttgtgctggc cgtgctgctc ccagttttat tcttgctcta ccggcaccgg 2460
aacagcatga aagtcttcct gaagcagggg gaatgtgcc aagcgtgcaccc caagacctgc 2520
cctgtggtgc tgcacctga gacccgccc ctcaacggcc tagggccccc tagcacccca 2580
ctcgatcacc gagggtagca gtccctgtca gacagccccc cgggggtcccg agtcttcact 2640
gagtcagaga agaggccact cagcatccaa gacagcttcg tggaggtatc cccagtgtgc 2700
ccccggcccc gggtcgcgct tggctcggag atccgtgact ctgtggtgtg agagctgact 2760
tccagaggac gctgccttg cttcaggggc tgtgaatgct cggagagggg caactggacc 2820
tcccctccgc tctgctcttc gtggaacacg accgtggtgc ccggcccttg ggagccttg 2880
ggccagctgg cctgctgctc tccagtcaag tagcgaagct cctaccaccc agacacccaa 2940
acagccgtgg cccagaggt cctggccaaa tatggggggc tgcctagggt ggtggaacag 3000
tgctccttat gtaaactgag ccctttgttt aaaaaacaat tccaaatgtg aaactagaat 3060
gagagggaag agatagcatg gcatgcagca cacacggctg ctccagttca tggcctcca 3120
ggggtgctgg ggatgcatcc aaagtgggtt tctgagacag agttggaac cctcaccaac 3180
tggcctcttc acctccaca ttatcccgct gccaccggct gccctgtctc actgcagatt 3240
caggaccagc ttgggctgcg tgcgttctgc cttgccagtc agccgaggat gtagttgttg 3300
ctgccgtcgt cccaccacct cagggaccag agggctagg tggcactgcg gccctacca 3360
ggctcctggc tcggacccaa ctctggacc tttccagcct gtatcaggct gtggccacac 3420
gagaggacag cgcgagctca ggagagattt cgtgacaatg tacgcctttc cctcagaatt 3480
cagggaagag actgtgcgct gccttcctcc gtgttgctg gagaaccctg gtgccccttc 3540
ccaccatatc caccctcgct ccatctttga actcaaacac gaggaactaa ctgcaccctg 3600
gtcctctccc cagtcaccag ttcacctcc atccctcacc ttcctccact ctaagggata 3660
tcaacactgc ccagcacagg ggcctgaat ttatgtggt tttatacatt ttttaataag 3720
atgcacttta tgtcattttt taataaagtc tgaagaatta ctgttt 3766

```

<210> 4

<211> 837

<212> PRT

<213> Human

<400> 4

```

Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro Trp
      5                      10                      15
Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu Leu Leu
      20                      25                      30
Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser Pro Arg Ile
      35                      40                      45
Ser Leu Pro Leu Gly Ser Glu Arg Pro Phe Leu Arg Phe Glu Ala
      50                      55                      60
Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu Ser Arg Asp Gly Arg
      65                      70                      75                      80
Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Leu Ser Ser Asn
      85                      90                      95
Leu Ser Phe Leu Pro Gly Gly Glu Tyr Gln Glu Leu Leu Trp Gly Ala
      100                     105                     110
Asp Ala Glu Lys Lys Gln Gln Cys Ser Phe Lys Gly Lys Asp Pro Gln
      115                     120                     125
Arg Asp Cys Gln Asn Tyr Ile Lys Ile Leu Leu Pro Leu Ser Gly Ser
      130                     135                     140
His Leu Phe Thr Cys Gly Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr
      145                     150                     155                     160
Ile Asn Met Glu Asn Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val
      165                     170                     175
Leu Leu Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys
      180                     185                     190
Ser Thr Ala Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ile

```

195						200						205			
Ser	Phe	Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg
210						215					220				
Pro	Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe
225					230					235					240
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly	Asp
				245					250				255		
Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu	Phe	Glu
			260					265				270			
Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile	Cys	Lys	Gly
		275				280				285					
Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp	Thr	Ser	Phe	Leu
	290					295				300					
Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp	Gly	Phe	Pro	Phe	Asn
305					310				315						320
Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro	Ser	Pro	Gln	Asp	Trp	Arg
			325						330						